

CLAIMS:

1. An adeno-associated virus (AAV) clade comprising at least three AAV members, wherein each member of said AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05.
2. The AAV clade according to claim 1, wherein the clade is selected from the group consisting of Clade E comprising as a member AAV8, Clade D comprising as a member AAV7, Clade F comprising as a member AAV9, Clade B comprising as a member AAV2, and Clade C comprising as a member H2.
3. The clade according to claim 1, wherein one or more of said AAV members is a non-naturally occurring AAV.
4. The clade according to claim 1, wherein two or more of said AAV members are naturally occurring AAV.
5. An adeno-associated virus (AAV) clade E comprising AAV8 and at least two additional AAV members, wherein each member of said AAV clade as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05.
6. The AAV Clade E according to claim 5, wherein one or more of said AAV members has a capsid with an amino acid identity of at least 85% with the capsid of AAV8, SEQ ID NO: 183.
7. The AAV Clade E according to claim 5, wherein said clade comprises at least AAV8 SEQ ID NO:183, 43.1/rh.2; rh. 4; rh.8; 44.2/rh.10; rh. 25; 29.3/bb.1; 29.5/bb.2; 30.10/pi.1 (SEQ ID NOs:28 and 93), 30.12/pi.2 (SEQ ID NOs:30 and 95), 30.19/pi.3 (SEQ ID NOs:29 and 94), LG-4/rh.38 (SEQ ID Nos: 7 and 86); LG-10/rh.40

(SEQ ID Nos: 14 and 92); N721-8/rh.43 (SEQ ID Nos: 43 and 163); 1-8/rh.49 (SEQ ID NOs: 25 and 103); 2-4/rh.50 (SEQ ID Nos: 23 and 108); 2-5/rh.51 (SEQ ID Nos: 22 and 104); 3-9/rh.52 (SEQ ID Nos: 18 and 96); 3-11/rh.53 (SEQ ID NOs: 17 and 97); 5-3/rh.57 (SEQ ID Nos: 26 and 105); 5-22/rh.58 (SEQ ID Nos: 27 and 58); modified rh. 58 (SEQ ID NO: 232); 2-3/rh.61 (SEQ ID NOs: 21 and 107); 4-8/rh.64 (SEQ ID Nos: 15 and 99); modified rh. 64 (SEQ ID NO: 233); 3.1/hu.6 (SEQ ID NO: 5 and 84); 33.12/hu.17 (SEQ ID NO: 4 and 83); 106.1/hu.37 (SEQ ID Nos: 10 and 88); LG-9/hu.39 (SEQ ID Nos: 24 and 102); 114.3/hu. 40 (SEQ ID Nos: 11 and 87); 127.2/hu.41 (SEQ ID NO: 6 and 91); 127.5/hu.42 (SEQ ID Nos: 8 and 85); hu. 66 (SEQ ID NOs: 173 and 197); modified rh.2 (SEQ ID NO: 231); and hu.67 (SEQ ID NOs: 174 and 198).

8. An AAV of clade E according to claim 5, provided that none of the AAV of said clade comprises a capsid of AAV8, 43.1/rh.2; rh. 4; rh.8; 44.2/rh.10; rh. 25; 29.3/bb.1; or 29.5/bb.2

9. The AAV of claim 8 selected from the group consisting of 30.10/pi.1 (SEQ ID NOs: 28 and 93), 30.12/pi.2 (SEQ ID NOs: 30 and 95), 30.19/pi.3 (SEQ ID NOs: 29 and 94), LG-4/rh.38 (SEQ ID Nos: 7 and 86); LG-10/rh.40 (SEQ ID Nos: 14 and 92); N721-8/rh.43 (SEQ ID Nos: 43 and 163); 1-8/rh.49 (SEQ ID NOs: 25 and 103); 2-4/rh.50 (SEQ ID Nos: 23 and 108); 2-5/rh.51 (SEQ ID Nos: 22 and 104); 3-9/rh.52 (SEQ ID Nos: 18 and 96); 3-11/rh.53 (SEQ ID NOs: 17 and 97); 5-3/rh.57 (SEQ ID Nos: 26 and 105); 5-22/rh.58 (SEQ ID Nos: 27 and 58); modified rh. 58 (SEQ ID NO: 232); 2-3/rh.61 (SEQ ID NOs: 21 and 107); 4-8/rh.64 (SEQ ID Nos: 15 and 99); modified rh. 64 (SEQ ID NO: 233); 3.1/hu.6 (SEQ ID NO: 5 and 84); 33.12/hu.17 (SEQ ID NO: 4 and 83); 106.1/hu.37 (SEQ ID Nos: 10 and 88); LG-9/hu.39 (SEQ ID Nos: 24 and 102); 114.3/hu. 40 (SEQ ID Nos: 11 and 87); 127.2/hu.41 (SEQ ID NO: 6 and 91); 127.5/hu.42 (SEQ ID Nos: 8 and 85); hu. 66 (SEQ ID NOs: 173 and 197); modified rh.2 (SEQ ID NO: 231); and hu.67 (SEQ ID NOs: 174 and 198).

10. An adeno-associated virus (AAV) clade D comprising AAV7 and least two additional AAV members, wherein each member of said AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap

value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05.

11. The AAV clade D according to claim 10, wherein said clade comprises at least AAV sources: AAV7; cy.2; cy.3; cy.4; cy.5; cy.6; rh.13; rh.37; rh. 36; rh.35; 2-15/ rh.62 (SEQ ID Nos: 33 and 114); 1-7/rh.48 (SEQ ID Nos: 32 and 115); 4-9/rh.54 (SEQ ID Nos: 40 and 116); and 4-19/rh.55 (SEQ ID Nos: 37 and 117) modified cy. 5 (SEQ ID NO: 227); modified rh.13 (SEQ ID NO: 228); and modified rh. 37 (SEQ ID NO: 229).

12. An AAV of the AAV clade D according to claim 10, provided that none of the AAV of said clade comprises a capsid of AAV7 SEQ ID NOs: 180 and 181; AAV7; cy.2; cy.3; cy.4; cy.5; cy.6; rh.13; rh.37; rh. 36; rh.35.

13. The AAV of claim 12 selected from the group consisting of 2-15/ rh.62 (SEQ ID Nos: 33 and 114); 1-7/rh.48 (SEQ ID Nos: 32 and 115); 4-9/rh.54 (SEQ ID Nos: 40 and 116); and 4-19/rh.55 (SEQ ID Nos: 37 and 117); modified cy. 5 (SEQ ID NO: 227); modified rh.13 (SEQ ID NO: 228); and modified rh. 37 (SEQ ID NO: 229).

14. An adeno-associated virus (AAV) clade B comprising AAV2 and least two additional AAV members, wherein each member of said AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05.

15. The AAV clade B according to claim 14, wherein said clade comprises at least AAV: AAV2, 52/hu.19 (SEQ ID NOs: 62 and 133), 52.1/hu.20 (SEQ ID NOs: 63 and 134), 54.5/hu.23 (SEQ ID Nos: 60 and 137), 54.2/hu.22 (SEQ ID Nos: 67 and 138), 54.7/hu.24 (SEQ ID Nos: 66 and 136), 54.1/hu.21 (SEQ ID Nos: 65 and 135), 54.4R/hu.27 (SEQ ID Nos: 64 and 140); 46.2/hu.28 (SEQ ID Nos: 68 and 130); 46.6/hu.29 (SEQ ID Nos: 69 and 132); modified hu. 29 (SEQ ID NO: 225); 172.1/hu.63 (SEQ ID NO: 171 and 195); 172.2/hu. 64 (SEQ ID NO: 172 and 196); 24.5/hu.13 (SEQ ID NO: 71 and 129); 145.6/hu.56 (SEQ ID NO: 168 and 192); hu.57 (SEQ ID Nos: 169

and 193); 136.1/hu.49 (SEQ ID NO: 165 and 189); 156.1/hu.58 (SEQ ID NO: 179 and 194); 72.2/hu.34 (SEQ ID NO: 72 and 125); 72.3/hu.35 (SEQ ID NO: 73 and 164); 129.1/hu.45 (SEQ ID NO: 76 and 127); 130.1/hu.47 (SEQ ID NO: 77 and 128); 140.1/hu.51 (SEQ ID NO: 161 and 190); and 140.2/hu.52 (SEQ ID NO: 167 and 191).

16. A member AAV of the AAV clade B according to claim 14, provided that none of the AAV of said clade comprises a capsid of AAV2.

17. The member AAV of claim 16 selected from the group consisting of 52/hu.19 (SEQ ID NOs: 62 and 133), 52.1/hu.20 (SEQ ID NOs: 63 and 134), 54.5/hu.23 (SEQ ID Nos: 60 and 137), 54.2/hu.22 (SEQ ID Nos: 67 and 138), 54.7/hu.24 (SEQ ID Nos: 66 and 136), 54.1/hu.21 (SEQ ID Nos: 65 and 135), 54.4R/hu.27 (SEQ ID Nos: 64 and 140); 46.2/hu.28 (SEQ ID Nos: 68 and 130); 46.6/hu.29 (SEQ ID Nos: 69 and 132); modified hu. 29 (SEQ ID NO: 225); 172.1/hu.63 (SEQ ID NO: 171 and 195); 172.2/hu. 64 (SEQ ID NO: 172 and 196); 24.5/hu.13 (SEQ ID NO: 71 and 129); 145.6/hu.56 (SEQ ID NO: 168 and 192); hu.57 (SEQ ID Nos: 169 and 193); 136.1/hu.49 (SEQ ID NO: 165 and 189); 156.1/hu.58 (SEQ ID NO: 179 and 194); 72.2/hu.34 (SEQ ID NO: 72 and 125); 72.3/hu.35 (SEQ ID NO: 73 and 164); 129.1/hu.45 (SEQ ID NO: 76 and 127); 130.1/hu.47 (SEQ ID NO: 77 and 128); 140.1/hu.51 (SEQ ID NO: 161 and 190); and 140.2/hu.52 (SEQ ID NO: 167 and 191).

18. An adeno-associated virus (AAV) clade A comprising AAV1, AAV6 and at least one additional member AAV, wherein each member of said AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05.

19. The AAV clade A according to claim 18, wherein said clade comprises at least AAV: AAV1; AAV6; 128.1/hu. 43; modified hu.43 (SEQ ID NO: 236); 128.3/hu. 44 (SEQ ID Nos: 81 and 158); hu.46 (SEQ ID NOs: 82 and 159); modified hu. 46 (SEQ ID NO: 224); and 130.4/hu.48 (SEQ ID NO: 78 and 157).

20. A member AAV of the AAV clade A according to claim 19, provided that none of the AAV of said clade comprises a capsid of AAV1 or AAV6.

21. The member AAV of claim 19 selected from the group consisting of 128.1/hu. 43; modified hu. 43 (SEQ ID NO: 236); 128.3/hu. 44 (SEQ ID Nos: 81 and 158); hu.46 (SEQ ID NOs: 82 and 159); modified hu. 46 (SEQ ID NO: 224); and 130.4/hu.48 (SEQ ID NO: 78 and 157).

22. An adeno-associated virus (AAV) clade C comprising A3.1/ch.5; H-6/hu.4; H-2/hu.2 and at least one further member AAV, wherein each member of said AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05.

23. The AAV clade C according to claim 21 wherein said clade comprises at least AAV: H-6/hu.4; H-2/hu.2; 3.1/hu.9 (SEQ ID Nos: 58 and 155); 16.8/hu.10 (SEQ ID Nos: 56 and 156); 16.12/hu.11 (SEQ ID Nos: 57 and 153); 145.1/hu.53 (SEQ ID Nos: 176 and 186); 145.6/hu.55 (SEQ ID Nos: 178 and 187); 145.5/hu.54 (SEQ ID Nos: 177 and 188); 7.3/hu.7 (SEQ ID Nos: 55 and 150); modified hu. 7 (SEQ ID NO: 226); 33.4/hu.15 (SEQ ID Nos: 50 and 147); 33.8/hu.16 (SEQ ID Nos: 51 and 148); 58.2/hu.25 (SEQ ID Nos: 49 and 146); 161.10/hu.60 (SEQ ID Nos: 170 and 184); H-5/hu.3 (SEQ ID Nos: 44 and 145); hu.18 (SEQ ID NOs: 52 and 149); H-1/hu.1 (SEQ ID Nos: 46 and 144); and 161.6/hu.61 (SEQ ID Nos: 174 and 185).

24. A member AAV of clade C according to claim 21, provided that none of the AAV of said clade comprises a capsid of A3.1/ch.5; H-6/hu.4; or H-2/hu.2.

25. The member AAV according to claim 24, wherein the AAV is selected from the group consisting of 3.1/hu.9 (SEQ ID Nos: 58 and 155); 16.8/hu.10 (SEQ ID Nos: 56 and 156); 16.12/hu.11 (SEQ ID Nos: 57 and 153); 145.1/hu.53 (SEQ ID Nos: 176 and 186); 145.6/hu.55 (SEQ ID Nos: 178 and 187); 145.5/hu.54 (SEQ ID Nos: 177 and 188); 7.3/hu.7 (SEQ ID Nos: 55 and 150); modified hu. 7 (SEQ ID NO: 226);

33.4/hu.15 (SEQ ID Nos: 50 and 147); 33.8/hu.16 (SEQ ID Nos: 51 and 148); 58.2/hu.25 (SEQ ID Nos: 49 and 146); 161.10/hu.60 (SEQ ID Nos: 170 and 184); H-5/hu.3 (SEQ ID Nos: 44 and 145); H-1/hu.1 (SEQ ID Nos: 46 and 144); hu.18 (SEQ ID NOs: 52 and 149); and 161.6/hu.61 (SEQ ID Nos: 174 and 185).

26. An adeno-associated virus (AAV) clade F comprising AAV9 and at least further two member AAV, wherein each member of said AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05.

27. The AAV clade F according to claim 26 wherein said clade comprises at least AAV hu.14/AAV9 (SEQ ID Nos: 3 and 123), hu.31 (SEQ ID NOs:1 and 121) and hu.32 (SEQ ID Nos: 2 and 122).

28. A member AAV of the AAV clade F according to claim 26.

29. The member AAV according to claim 28, wherein the AAV is selected from the group consisting of hu.14/AAV9 (SEQ ID Nos: 3 and 123), hu.31 (SEQ ID NOs:1 and 121) and hu.32 (SEQ ID Nos: 2 and 122).

30. An adeno-associated virus (AAV) of serotype 9 comprising an AAV capsid and a heterologous molecule for delivery to a cell,
wherein the AAV capsid is serologically related to a capsid of the sequence of amino acids 1 to 736 of SEQ ID NO: 123 and serologically distinct from a capsid protein of any of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7 or AAV8.

31. The AAV according to claim 30, wherein said virus has the nucleic acid sequence of SEQ ID NO: 3.

32. The AAV according to claim 30, wherein said AAV further comprises a minigene having AAV inverted terminal repeats and the heterologous gene operably linked to regulatory sequences which direct its expression in a host cell.

33. A protein comprising an AAV9/HU.14 protein or a fragment thereof selected from the group consisting of:

(a) an AAV9/HU.14 capsid protein or fragment thereof, selected from the group consisting of:

vp1 capsid protein, amino acids (aa) 1 to 736, SEQ ID NO:123;

vp2 capsid protein, aa 138 to 736, SEQ ID NO: 123 ;

vp3 capsid protein, aa 203 to 736, SEQ ID NO: 123;

a fragment encompassing hypervariable region (HVR)1 through 12 or a smaller fragment thereof selected the group consisting of: aa 146 to 152; aa 182 to 187; aa 262 to 264; aa 263 to 266; aa 263 to 266; aa 381 to 383; 383 to 385; aa 450 to 474; aa 451 to 475; aa 490 to 495; aa 491 to 496; aa500 to 504; aa 501 to 505; aa 514 to 522; aa 533 to 554; aa 534 to 555; aa 581 to 594; aa 583 to 596; aa 658 to 667; aa 660 to 669; and aa 705 to 719; aa 707 to 723;

aa 24 to 42, aa 25 to 28; aa 81 to 85; aa133 to 165; aa 134 to 165; aa 137 to 143; aa 154 to 156; aa 194 to 208; aa 261 to 274; aa 262 to 274; aa 171 to 173; aa 185 to 198; aa 413 to 417; aa 449 to 478; aa 494 to 525; aa 534 to 571; aa 581 to 601; aa 660 to 671; aa 709 to 723; and

aa 1 to 184, aa 199 to 259; aa 274 to 446; aa 603 to 659; aa 670 to 706; aa 724 to 736; aa 185 to 198; aa 260 to 273; aa447 to 477; aa495 to 602; aa603 to 659; aa 660 to 669; and aa707 to 723, wherein the amino acid numbers are those of the AAV2 capsid, SEQ ID NO:4 and corresponding regions in the capsid of AAV9/HU.14, SEQ ID NO:123.

34. An artificial adeno-associated virus (AAV) capsid protein comprising one or more of the AAV9/HU.14 capsid protein fragments according to claim 33a.

35. A recombinant adeno-associated virus (AAV) comprising an artificial capsid according to claim 34.

36. A molecule comprising a nucleic acid sequence encoding a protein according to claim 34.

37. The molecule according to claim 36, wherein said nucleic acid sequence is selected from the group consisting of:

vp1, nt 1 to 2211;

vp2, nt 2532 to 2211; and

vp 3, nt 2730 to 2211;

wherein the nucleotides numbers are of AAV9/HU.14, SEQ ID NO: 3.

38. The molecule according to claim 37, wherein said molecule comprises an AAV sequence encoding an AAV capsid protein and a functional AAV rep protein.

39. The molecule according to claim 37, wherein said molecule is a plasmid.

40. A method of generating a recombinant adeno-associated virus (AAV) comprising an AAV capsid comprising the steps of culturing a host cell containing: (a) a molecule encoding an AAV capsid protein; (b) a functional rep gene; (c) a minigene comprising AAV inverted terminal repeats (ITRs) and a transgene; and (d) sufficient helper functions to permit packaging of the minigene into the AAV capsid protein, wherein said host cell comprises a molecule according to claim 37.

41. A host cell transfected with an adeno-associated virus according to claim 30.

42. A host cell transfected with a molecule according to claim 33.

43. A composition comprising an AAV according to claim 30 and a physiologically compatible carrier.

44. A composition comprising a molecule according to claim 36 and a physiologically compatible carrier.
45. A method of delivering a transgene to a cell, said method comprising the step of contacting the cell with an AAV according to claim 30, wherein said rAAV comprises the transgene.
46. A non-naturally occurring adeno-associated virus (AAV) comprising an AAV capsid having an amino acid sequence selected from the group consisting of:
 30.10/pi.1 (SEQ ID NO: 93), 30.12/pi.2 (SEQ ID NO: 95), 30.19/pi.3 (SEQ ID NO: 94), LG-4/rh.38 (SEQ ID No: 86); LG-10/rh.40 (SEQ ID No: 92); N721-8/rh.43 (SEQ ID No: 163); 1-8/rh.49 (SEQ ID NO: 103); 2-4/rh.50 (SEQ ID No: 108); 2-5/rh.51 (SEQ ID No: 104); 3-9/rh.52 (SEQ ID No: 96); 3-11/rh.53 (SEQ ID NO: 97); 5-3/rh.57 (SEQ ID No: 105); 5-22/rh.58 (SEQ ID No: 58); 2-3/rh.61 (SEQ ID NO: 107); 4-8/rh.64 (SEQ ID No: 99); 3.1/hu.6 (SEQ ID NO: 84); 33.12/hu.17 (SEQ ID NO: 83); 106.1/hu.37 (SEQ ID No: 88); LG-9/hu.39 (SEQ ID No: 102); 114.3/hu.40 (SEQ ID No: 87); 127.2/hu.41 (SEQ ID NO: 91); 127.5/hu.42 (SEQ ID No: 85); hu.66 (SEQ ID NO: 197); modified rh.2 (SEQ ID NO: 231); and hu.67 (SEQ ID NO: 198) from Clade E;
 2-15/ rh.62 (SEQ ID No: 114); 1-7/rh.48 (SEQ ID No: 115); 4-9/rh.54 (SEQ ID No: 116); and 4-19/rh.55 (SEQ ID No: 117); modified cy. 5 (SEQ ID NO: 227); modified rh.13 (SEQ ID NO: 228); and modified rh.37 (SEQ ID NO: 229) from the clade D; 52/hu.19 (SEQ ID NO: 133), 52.1/hu.20 (SEQ ID NO: 134), 54.5/hu.23 (SEQ ID No: 137), 54.2/hu.22 (SEQ ID No: 138), 54.7/hu.24 (SEQ ID No: 136), 54.1/hu.21 (SEQ ID No: 135), 54.4R/hu.27 (SEQ ID No: 140); 46.2/hu.28 (SEQ ID No: 130); 46.6/hu.29 (SEQ ID No: 132); modified hu.29 (SEQ ID NO: 225); 172.1/hu.63 (SEQ ID NO: 195); 172.2/hu.64 (SEQ ID NO: 196); 24.5/hu.13 (SEQ ID NO: 129); 145.6/hu.56 (SEQ ID NO: 192); hu.57 (SEQ ID No: 193); 136.1/hu.49 (SEQ ID NO: 189); 156.1/hu.58 (SEQ ID NO: 194); 72.2/hu.34 (SEQ ID NO: 125); 72.3/hu.35 (SEQ ID NO: 164); 129.1/hu.45 (SEQ ID NO: 127); 130.1/hu.47 (SEQ ID NO: 128); 140.1/hu.51 (SEQ ID NO: 190); and 140.2/hu.52 (SEQ ID NO: 191) from clade B;

128.1/hu. 43 (SEQ ID Nos: 160); modified hu. 43 (SEQ ID NO: 236); 128.3/hu. 44 (SEQ ID Nos: 158); hu.46 (SEQ ID NO: 159); modified hu.46 (SEQ ID NO: 224); and 130.4/hu.48 (SEQ ID NO: 157) from Clade A;

3.1/hu.9 (SEQ ID Nos: 155); 16.8/hu.10 (SEQ ID Nos: 156); 16.12/hu.11 (SEQ ID Nos: 153); 145.1/hu.53 (SEQ ID No: 186); 145.6/hu.55 (SEQ ID No: 187); 145.5/hu.54 (SEQ ID No: 188); 7.3/hu.7 (SEQ ID No: 150); modified hu. 7 (SEQ ID NO: 226); 33.4/hu.15 (SEQ ID No: 147); 33.8/hu.16 (SEQ ID No: 148); 58.2/hu.25 (SEQ ID No: 146); 161.10/hu.60 (SEQ ID No: 184); H-5/hu.3 (SEQ ID No: 145); H-1/hu.1 (SEQ ID No: 144); hu.18 (SEQ ID NOs: 52 and 149); and 161.6/hu.61 (SEQ ID No: 185) from Clade C;

hu.31 (SEQ ID NO: 121) and hu.32 (SEQ ID No: 122) from Clade F; and rh.59 (SEQ ID NO: 110) and rh.60 (SEQ ID NO: 120); or a unique, functional fragment thereof.

47. The AAV according to claim 46, wherein the fragment is selected from the group consisting of:

a fragment encompassing hypervariable region (HVR)1 through 12 or a smaller fragment thereof selected the group consisting of: aa 146 to 152; aa 182 to 187; aa 262 to 264; aa 263 to 266; aa 263 to 266; aa 381 to 383; 383 to 385; aa 450 to 474; aa 451 to 475; aa 490 to 495; aa 491 to 496; aa500 to 504; aa 501 to 505; aa 514 to 522; aa 533 to 554; aa 534 to 555; aa 581 to 594; aa 583 to 596; aa 658 to 667; aa 660 to 669; and aa 705 to 719; aa 707 to 723;

aa 24 to 42, aa 25 to 28; aa 81 to 85; aa133 to 165; aa 134 to 165; aa 137 to 143; aa 154 to 156; aa 194 to 208; aa 261 to 274; aa 262 to 274; aa 171 to 173; aa 185 to 198; aa 413 to 417; aa 449 to 478; aa 494 to 525; aa 534 to 571; aa 581 to 601; aa 660 to 671; aa 709 to 723; and

aa 1 to 184, aa 199 to 259; aa 274 to 446; aa 603 to 659; aa 670 to 706; aa 724 to 736; aa 185 to 198; aa 260 to 273; aa447 to 477; aa495 to 602; aa603 to 659; aa 660 to 669; and aa707 to 723,

wherein the amino acid numbers are those of the AAV2 capsid, SEQ ID NO:4 and corresponding regions in the capsid of 30.10/pi.1 (SEQ ID NO: 93), 30.12/pi.2 (SEQ ID NO: 95), 30.19/pi.3 (SEQ ID NO: 94), LG-4/rh.38 (SEQ ID No: 86);

LG-10/rh.40 (SEQ ID No: 92); N721-8/rh.43 (SEQ ID No: 163); 1-8/rh.49 (SEQ ID NO: 103); 2-4/rh.50 (SEQ ID No: 108); 2-5/rh.51 (SEQ ID No: 104); 3-9/rh.52 (SEQ ID No: 96); 3-11/rh.53 (SEQ ID NO: 97); 5-3/rh.57 (SEQ ID No: 105); 5-22/rh.58 (SEQ ID No: 58); modified rh. 58 (SEQ ID NO: 232); 2-3/rh.61 (SEQ ID NO: 107); 4-8/rh.64 (SEQ ID No: 99); modified rh. 64 (SEQ ID NO: 233); 3.1/hu.6 (SEQ ID NO: 84); 33.12/hu.17 (SEQ ID NO: 83); 106.1/hu.37 (SEQ ID No: 88); LG-9/hu.39 (SEQ ID No: 102); 114.3/hu. 40 (SEQ ID No: 87); 127.2/hu.41 (SEQ ID NO: 91); 127.5/hu.42 (SEQ ID No: 85); hu. 66 (SEQ ID NO: 197); modified rh.2 (SEQ ID NO:231); and hu.67 (SEQ ID NO: 198) from clade E;

2-15/ rh.62 (SEQ ID No: 114); 1-7/rh.48 (SEQ ID No: 115); 4-9/rh.54 (SEQ ID No: 116); and 4-19/rh.55 (SEQ ID No: 117); modified cy. 5 (SEQ ID NO: 227); modified rh.13 (SEQ ID NO: 228); and modified rh. 37 (SEQ ID NO: 229) from clade D; 52/hu.19 (SEQ ID NO: 133), 52.1/hu.20 (SEQ ID NO: 134), 54.5/hu.23 (SEQ ID No: 137), 54.2/hu.22 (SEQ ID No: 138), 54.7/hu.24 (SEQ ID No: 136), 54.1/hu.21 (SEQ ID No: 135), 54.4R/hu.27 (SEQ ID No: 140); 46.2/hu.28 (SEQ ID No: 130); 46.6/hu.29 (SEQ ID No: 132); modified hu. 29 (SEQ ID NO: 225); 172.1/hu.63 (SEQ ID NO: 195); 172.2/hu. 64 (SEQ ID NO: 196); 24.5/hu.13 (SEQ ID NO: 129); 145.6/hu.56 (SEQ ID NO: 192); hu.57 (SEQ ID No: 193); 136.1/hu.49 (SEQ ID NO: 189); 156.1/hu.58 (SEQ ID NO: 194); 72.2/hu.34 (SEQ ID NO: 125); 72.3/hu.35 (SEQ ID NO: 164); 129.1/hu.45 (SEQ ID NO: 127); 130.1/hu.47 (SEQ ID NO: 128); 140.1/hu.51 (SEQ ID NO: 190); and 140.2/hu.52 (SEQ ID NO: 191) from clade B;

128.1/hu. 43 (SEQ ID Nos: 160); modified hu. 43 (SEQ ID NO: 236); 128.3/hu. 44 (SEQ ID Nos: 158); hu.46 (SEQ ID NO: 159); modified hu. 46 (SEQ ID NO: 224); and 130.4/hu.48 (SEQ ID NO: 157) from Clade A;

3.1/hu.9 (SEQ ID Nos: 155); 16.8/hu.10 (SEQ ID Nos: 156); 16.12/hu.11 (SEQ ID Nos: 153); 145.1/hu.53 (SEQ ID No: 186); 145.6/hu.55 (SEQ ID No: 187); 145.5/hu.54 (SEQ ID No: 188); 7.3/hu.7 (SEQ ID No: 150); modified hu. 7 ([SEQ ID NO: 226); 33.4/hu.15 (SEQ ID No: 147); 33.8/hu.16 (SEQ ID No: 148); 58.2/hu.25 (SEQ ID No: 146); 161.10/hu.60 (SEQ ID No: 184); H-5/hu.3 (SEQ ID No: 145); H-1/hu.1 (SEQ ID No: 144); hu.18 (SEQ ID NO: 149) and 161.6/hu.61 (SEQ ID No: 185) from Clade C;

hu.31 (SEQ ID NO: 121) and hu.32 (SEQ ID No: 122) from Clade F; and

rh.59 (SEQ ID NO: 110) and rh.60 (SEQ ID NO: 120),.

48. An artificial adeno-associated virus (AAV) capsid protein comprising one or more of the AAV capsid protein fragments according to claim 47a.

49. A recombinant adeno-associated virus (AAV) comprising an artificial capsid according to claim 48.

50. A molecule comprising a heterologous nucleic acid sequence encoding an AAV capsid protein, wherein said nucleic acid sequence is selected from the group consisting of:

30.10/pi.1 (SEQ ID NO: 28), 30.12/pi.2 (SEQ ID NO: 30), 30.19/pi.3 (SEQ ID NO: 29), LG-4/rh.38 (SEQ ID No: 7); LG-10/rh.40 (SEQ ID No: 14); N721-8/rh.43 (SEQ ID No: 43); 1-8/rh.49 (SEQ ID NO: 25); 2-4/rh.50 (SEQ ID No: 23); 2-5/rh.51 (SEQ ID No: 22); 3-9/rh.52 (SEQ ID No: 18); 3-11/rh.53 (SEQ ID NO: 17); 5-3/rh.57 (SEQ ID No: 26); 5-22/rh.58 (SEQ ID No: 27); modified rh. 58 (SEQ ID NO: 232); 2-3/rh.61 (SEQ ID NO: 21); 4-8/rh.64 (SEQ ID No: 15); 3.1/hu.6 (SEQ ID NO: 5); 33.12/hu.17 (SEQ ID NO:4); 106.1/hu.37 (SEQ ID No: 10); LG-9/hu.39 (SEQ ID No: 24); 114.3/hu. 40 (SEQ ID No: 11); 127.2/hu.41 (SEQ ID NO:6); 127.5/hu.42 (SEQ ID No: 8); hu. 66 (SEQ ID NO: 173); modified rh.2 (SEQ ID NO:231); and hu.67 (SEQ ID NO: 174) from Clade E;

2-15/ rh.62 (SEQ ID No: 33); 1-7/rh.48 (SEQ ID No: 32); 4-9/rh.54 (SEQ ID No: 40); and 4-19/rh.55 (SEQ ID Nos: 37 and 117); modified cy. 5 (SEQ ID NO: 227); modified rh.13 (SEQ ID NO: 228); and modified rh. 37 (SEQ ID NO: 229) from Clade D;

52/hu.19 (SEQ ID NOs: 62 and 133), 52.1/hu.20 (SEQ ID NOs: 63 and 134), 54.5/hu.23 (SEQ ID No: 60), 54.2/hu.22 (SEQ ID No: 67), 54.7/hu.24 (SEQ ID No: 66), 54.1/hu.21 (SEQ ID No: 65), 54.4R/hu.27 (SEQ ID No: 64); 46.2/hu.28 (SEQ ID No: 68); 46.6/hu.29 (SEQ ID No: 69); modified hu. 29 (SEQ ID NO: 225); from Clade B;

128.1/hu. 43 (SEQ ID No: 80); 128.3/hu. 44 (SEQ ID No: 81); hu.46 (SEQ ID NOs: 82) and 130.4/hu.48 (SEQ ID NO: 78) from Clade A;
3.1/hu.9 (SEQ ID No: 58); 16.8/hu.10 (SEQ ID No: 56);
16.12/hu.11 (SEQ ID No: 57); 145.1/hu.53 (SEQ ID No: 176); 145.6/hu.55 (SEQ ID No: 178); 145.5/hu.54 (SEQ ID No: 177); 7.3/hu.7 (SEQ ID No: 55); modified hu.7 (SEQ ID NO: 226); 33.4/hu.15 (SEQ ID No: 50); 33.8/hu.16 (SEQ ID No: 51); 58.2/hu.25 (SEQ ID No: 49); 161.10/hu.60 (SEQ ID No: 170); H-5/hu.3 (SEQ ID No: 44); hu.18 (SEQ ID NO: 149); H-1/hu.1 (SEQ ID No: 46); and 161.6/hu.61 (SEQ ID No: 174) from Clade C;
hu.14/AAV9 (SEQ ID No: 3), hu.31 (SEQ ID NO:1) and hu.32 (SEQ ID No: 2) from Clade F;
rh.59 (SEQ ID NO: 49) and rh.60 (SEQ ID NO: 31);
or a unique, functional fragment thereof.

51. The molecule according to claim 50, wherein said molecule comprises an AAV sequence encoding an AAV capsid protein and a functional AAV rep protein.

52. The molecule according to claim 50, wherein said molecule is a plasmid.

53. A method of generating a recombinant adeno-associated virus (AAV) comprising an AAV capsid comprising the steps of culturing a host cell containing: (a) a molecule encoding an AAV capsid protein; (b) a functional rep gene; (c) a minigene comprising AAV inverted terminal repeats (ITRs) and a transgene; and (d) sufficient helper functions to permit packaging of the minigene into the AAV capsid protein, wherein said host cell comprises a molecule according to claim 50.

54. A host cell transfected with an adeno-associated virus according to claim 30.

55. A host cell transfected with a molecule according to claim 50.

56. A composition comprising an AAV according to claim 47 and a physiologically compatible carrier.

57. A composition comprising a molecule according to claim 50 and a physiologically compatible carrier.

58. A method of delivering a transgene to a cell, said method comprising the step of contacting the cell with an AAV according to claim 47, wherein said rAAV comprises the transgene.